

cagctacatg ccattaatct ggaaggaacg ggcaggaaag ccaccatgca aacaaccag
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 gagcgaatga tgaaggatgt cttctttttc ctcttcttcc tgagcgtatg gcttgtggcc
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 cgccgtgtgc tatacaggcc ttacctgcag atctttgggc aaatccctct ggatgaaatt
 gatgaggctc gtgtgaactg ttctcttcac cctctgctgc tggaaagctc ggcttctgc
 cctaattctc atgccaactg gctggtcatt ctctgctgg ttaccttctc gcttgtcact

FIG. 1A

[illegible]

FIG. 1 B

MQTTQSSCPGPPDTEGWEPILCRGEINFGSGKKRGKFKVPSSVAPSVLFELLTEWHLPAPNLVVSLVGEERPLAMKSWLRDVLK
 KGLVKAAQSTGAWILTSALHVGGLARHVGQAVRDHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDTPIHYPADEGNIQGPLCPL
 DSNLSHFILVESGALGSGNDGLTELQSLSEKHISQORTGYGGTSCIPIVCLLVNGDPNTLERISRAVEQAAPWILAGSGGIADVLA
 ALVSQPHLLVPQVAEKQFREKFPSECFSEWAIVHWTELLQNIAAHPHLLTVYDFEQEGSEDLDTVILKALVKACKSHSQEAQDYLDLKL
 LAVAWDRVDIAKSEIFNGDVVEWKSCDLEEVMTDALVSNKPDFVRLFVDSGADMAEFLTYGRLLQLYHSVSPKSLFELLQRKHEEGRLT
 LAGLGAQQARELP IGLPAFSLHVSRLKDFLHDACRGFYQDGRMEERGPPKRPAGQKWL PDL SRKSEDPWRDLFLWAVLQNR YEMATY
 FWAMGREGVAAALAAACKIIKEMSHLEKEAEVARTMREAKYEQALDLFSECYGNSEDRAFALLVRRNHSWRTTCLHLATEADAKAFFA
 HDGVQAFLLTKIWWGDMATGTPILRLLGAFTCPALITYTNLISFSEDAPQRMDELDQEPDSDMEKSFLCSRGQLEKL TEAPRAPGDLG
 PQAAFLLLTRWRKFWGAPVTVFLGNVVMYFAFLFLFTYVLLVDFRPPQPGPSGSEVTL YFWVFTLVLEEIRQGFFTDETHLVKKFTLYV
 EDNWNKCDMVAIFLFI VGTCTRMVPSVFEAGRTVLAIDFMVFTLR LIHIFAIHKQLGPKII IVERMMKDVFFFLLFVSVWLVA YGVTTQ
 ALLHPHGRLEWIFRRVLYRPLYQIFGQIPLDEIDEARVNC SLHPLLESSASCPNL YANWLVI LLLVTFLLVTNVLLMNLIIAMFSYT
 FQVVQGNADMFWKQRYHL IVEYHGRPALAPPFILLSHLSLVLKQVFRKEAQHKRQHLE RDL PDL DQKIITWETVQKENFLSTMEKRR
 RDSEGEVLRKTAHRVDLIAKYIGGLREQEKRIKCLSEQANYCM LLLSSMTDTLAPGGTYSSSQNGCRSQPASARDREYLESGLPSPSDT

FIG.2

atgcaggatg tccaaggccc ccgtcccgga agccccgggg atgctgaaga ccggcgggag
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 atcccactgg catcctgccc cagcctctat gccaaactggc tggtcatcct cctgctggtc
 gaggactcac tggtcacaa tgtgctgctc atgaacctgc tcacgccat gttcagctac
 accttctgt tgggtcaggg caacgcagac atgttctgga agttccagcg ctacaacctg

FIG.3A

[illegible][illegible]

FIG. 4

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mTrp8	MQTTQSSCPGSPDTEGWEPILCRGEINFGGSGKKRGKFKVKVPSSVAPSVLFELLTEW	60
hTRP8	MQDVQGPRPGSPGDAEDRRELGLHRGEVNFGGSGKKRGKFKVRVPSPGVAPSVLFDLLAEW	60
	** . * . . ***** * . ** * * *** . ***** . *** . ***** . *** . **	
mTrp8	HLPAPNLVVSLVGEERPLAMKSWLRDVLRKGLVKAAQSTGAWILTSALHVGLARHVGQAV	120
hTRP8	HLPAPNLVVSLVGEEQPFAMKSWLRDVLRKGLVKAAQSTGAWILTSALRVGLARHVGQAV	120
	***** . * . ***** . ***** . ***** . ***** . ***** . *****	
mTrp8	RDHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQKEDTPIHYPADegNIQGPlCPLDS	180
hTRP8	RDHSLASTSTKVRVAVGMASLGRVLHRRILEEAQ - - EDFPVHYPEDDGGSQGPlCSLDS	178
	***** . ***** . ***** . * . *** : . * : . : ** * . *** * . * . ***** . ***	
mTrp8	NLSHFILVESGALGSGNDGLTELQLSLEKHISQQRGTGYGGTSCIQIPVLCLLVNGDPNTL	240
hTRP8	NLSHFILVEPGPPGKG - DGLTELRLRLEKHISEQRAGYGGTGSIEIPVLCLLVNGDPNTL	237
	***** . * . * . * ***** . * ***** . ** . ***** . . * . ***** . *****	
mTrp8	ERISRAVEQAAPWLILAGSGGIADVLAALVSQPHLLVPQVAEKQFREKFPSECFSEWAIIV	300
hTRP8	ERISRAVEQAAPWLILVGSGGIADVLAALVNQPHLLVPKVAEKQFKEKFPSEKHFSEWEDIV	297
	***** . ***** . ***** . ***** . ***** . ***** . *****	
mTrp8	HWTELLQNIAAHPHLLTVYDFEQEGSELDTVILKALVKACKSHSQAQDYLDLKLAVA	360
hTRP8	RWTKLLQNITSHQHLLTVYDFEQEGSELDTVILKALVKACKSHSQEPQDYLDLKLAVA	357
	: ** . ***** : . * ***** . ***** . ***** . ***** . *****	
mTrp8	WDRVDIAKSEIFNGDVEWKSCDLEEVMTDALVSNKPDFVRLFVDSGADMAEFLTYGRLQQ	420
hTRP8	WDRVDIAKSEIFNGDVEWKSCDLEEVMDALVSNKPEFVRLFVDNGADVADFLTYGRLQE	417
	***** . ***** . ***** . ***** . *** . * . ***** .	
mTrp8	LYHSVSPKSLLFELLQRKHEEGRLTLAGLGAQQARELPIGLPAFSLHEVSRVLKDFLHDA	480
hTRP8	LYRSVSRKSLLFDLLQRKQEEARLTLAGLGTQQAREPPAGPPAFSLHEVSRVLKDFLQDA	477
	** . *** ***** . ***** . ** . ***** . ***** * * ***** . **	
mTrp8	CRGFYQDGR - - - RMEERGPPKRPAGQKWLPDLSRKSEDPWRDLFLWAVLQNRHYEMATYF	536
hTRP8	CRGFYQDGRPGDRRAEKGPAPKPTGQKWLLDNQKSENPNWRDLFLWAVLQNRHEMATYF	537
	***** * * . ** . *** . ***** ** . : *** . ***** . *****	
mTrp8	WAMGREGVAAALAACKIIKEMSHLEKEAEVARTMREAKYEQALDLFSECYGNSEDRAFA	596
hTRP8	WAMGQEGVAAALAACKILKEMSHLETEAEARATREAKYERLALDLFSECYSNSEARAF	597
	**** . ***** . ***** . *** . ** : ***** . ***** . *** *****	

FIG.5

Classification and Secondary Structure Prediction of Membrane Proteins

<http://azusa.proteome.bio.tuat.ac.jp/sosui/>

Orientation of the N-terminus of	mTrp8:	IN		
Number of transmembrane helices of	mTrp8:	6		
Position of transmembrane helices of	mTrp8:	helix	begin	end
		1	732	754
		2	769	792
		3	807	829
		4	839	863
		5	870	893
		6	955	977

Orientation of the N-terminus of	hTrp8:	IN		
Number of transmembrane helices of	hTrp8:	6		
Position of transmembrane helices of	hTrp8:	helix	begin	end
		1	733	755
		2	770	792
		3	807	829
		4	843	863
		5	873	893
		6	955	977

FIG.6A

HYDROPHOBICITY PROFILE OF mTrp8 (MADE WITH DNAMAN SOFTWARE)

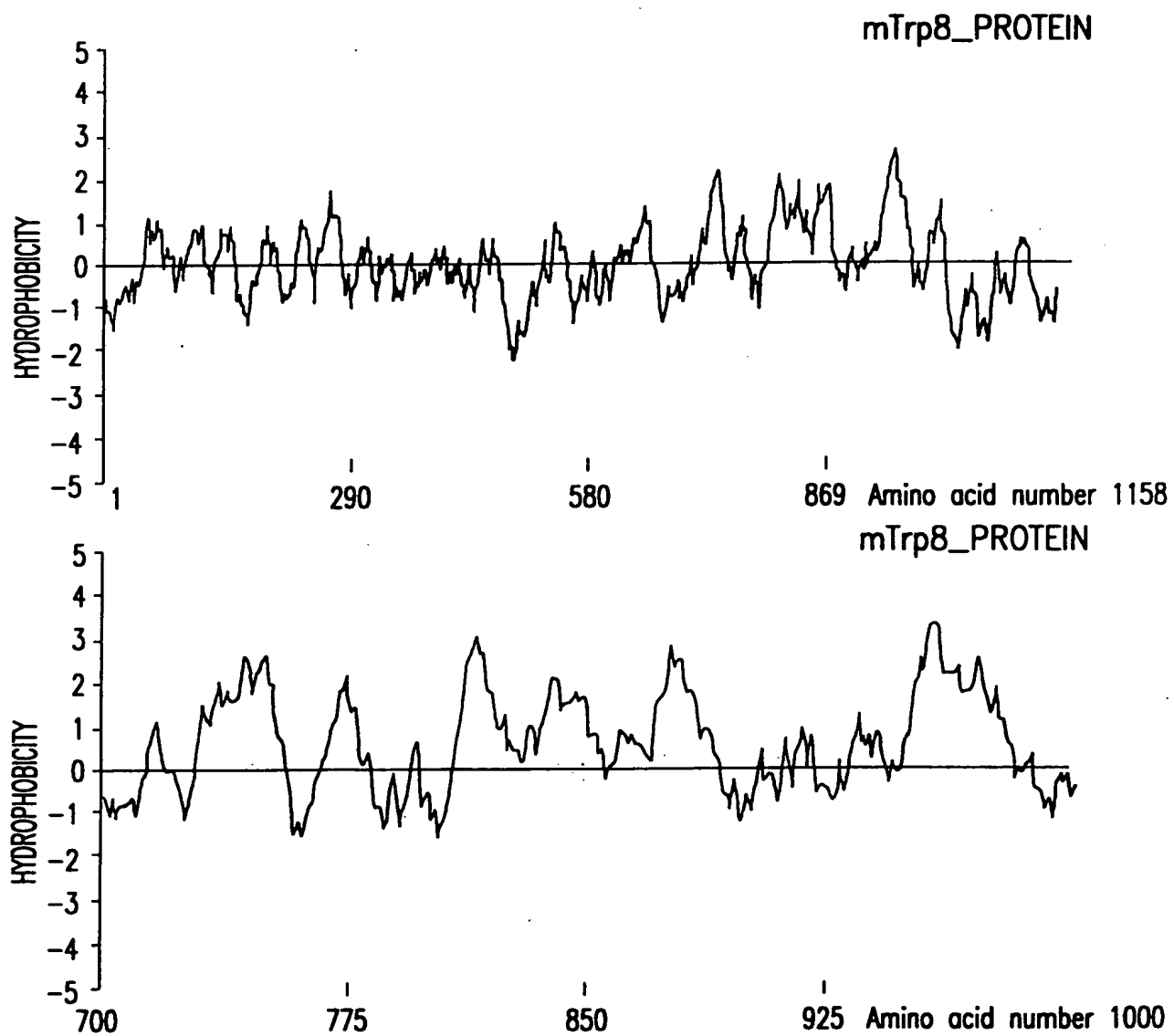


FIG. 6B

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HYDROPHOBICITY PROFILE OF hTrp8 (MADE WITH DNAMAN SOFTWARE)

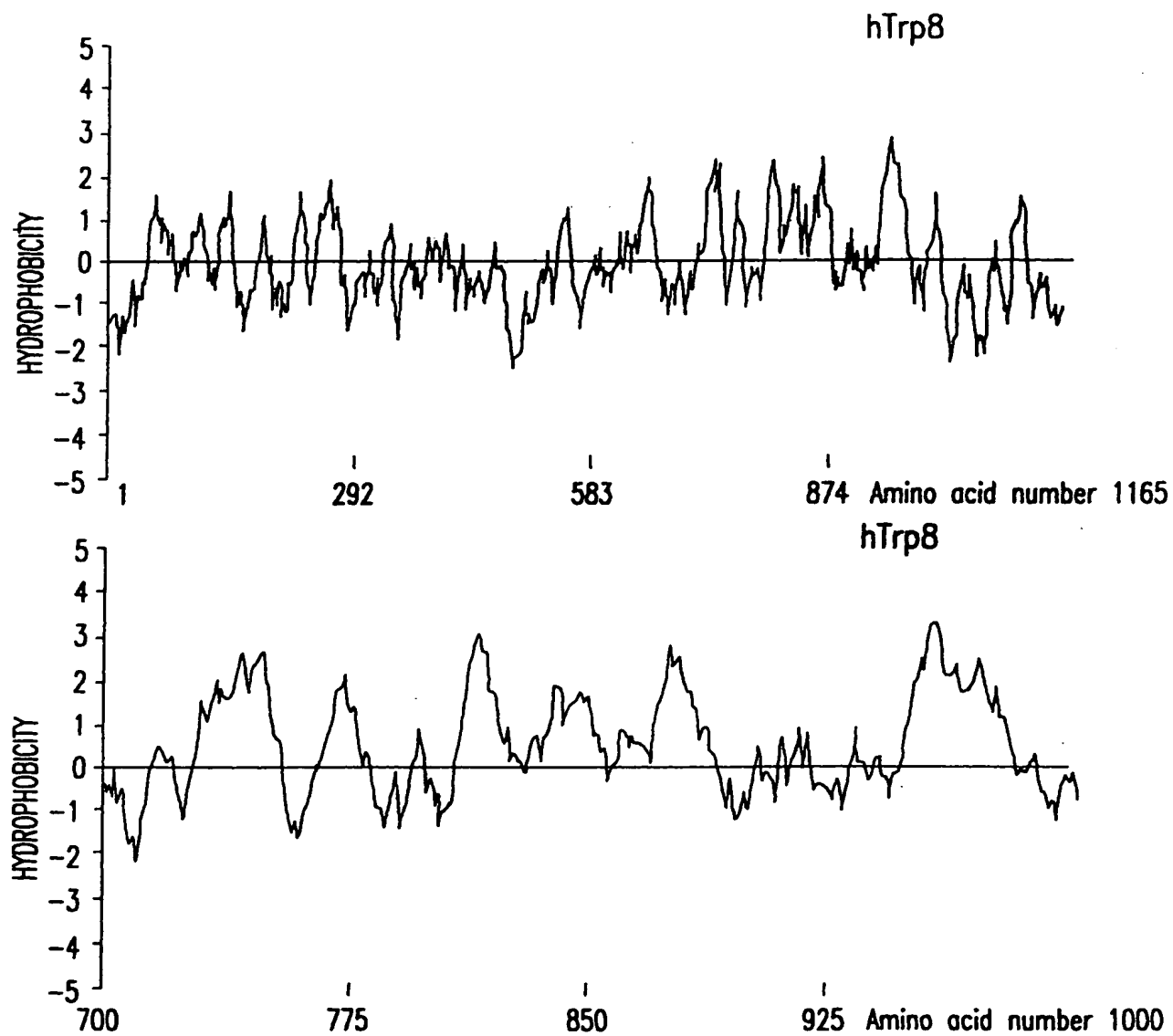


FIG. 6C

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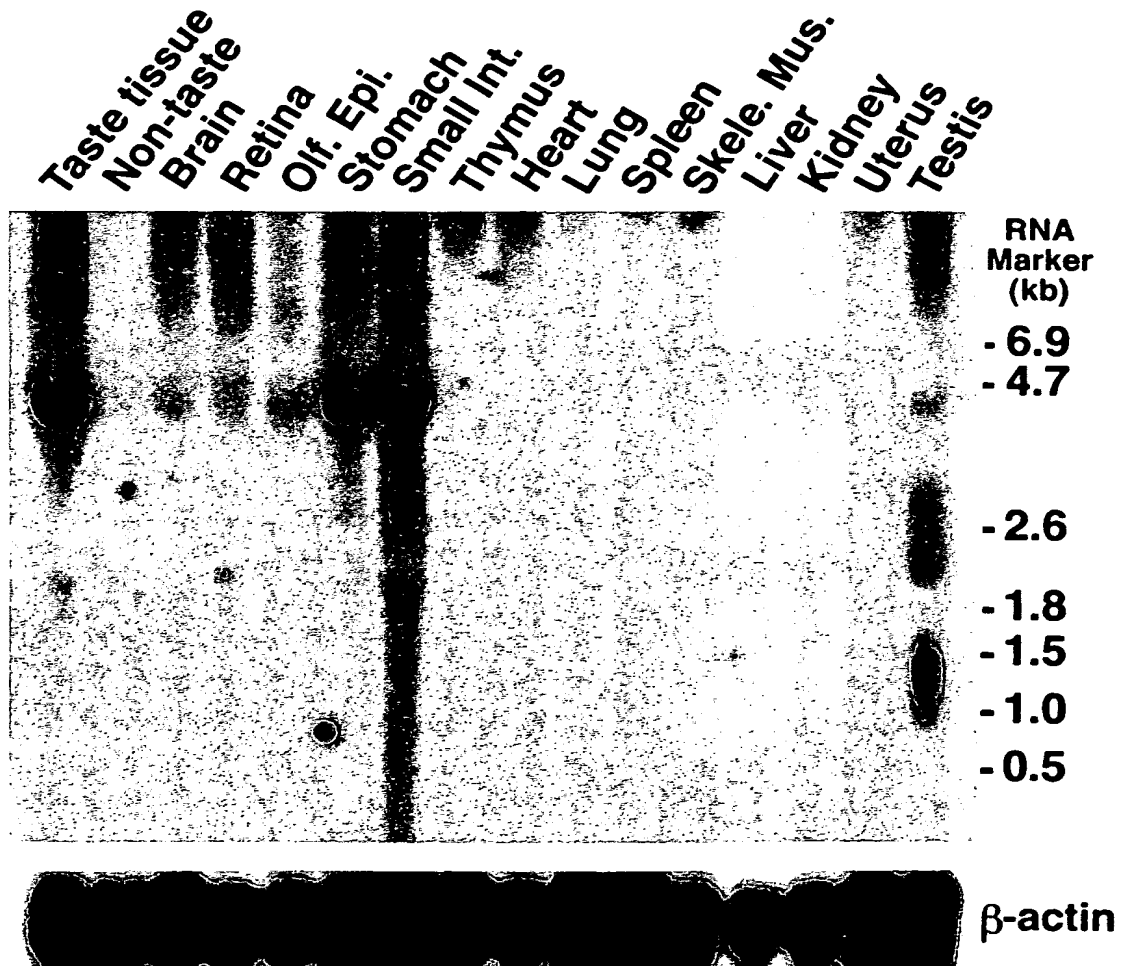


FIG.7

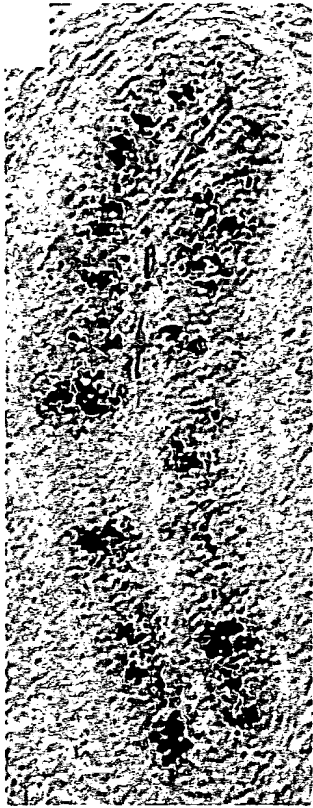


FIG.8A

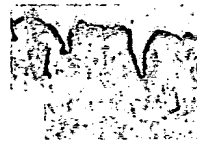


FIG.8E



FIG.8B



FIG.8C

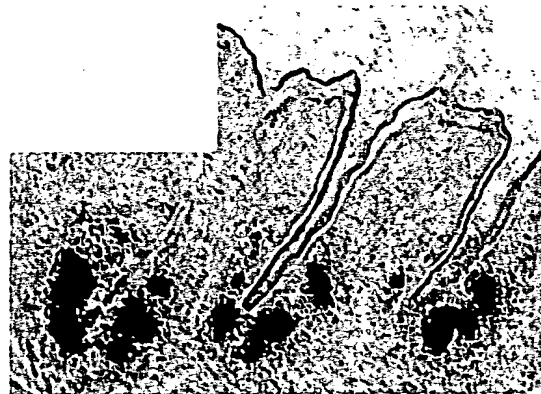


FIG.8D

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FIG.9G



FIG.9H



FIG.9I

FIG. 9G

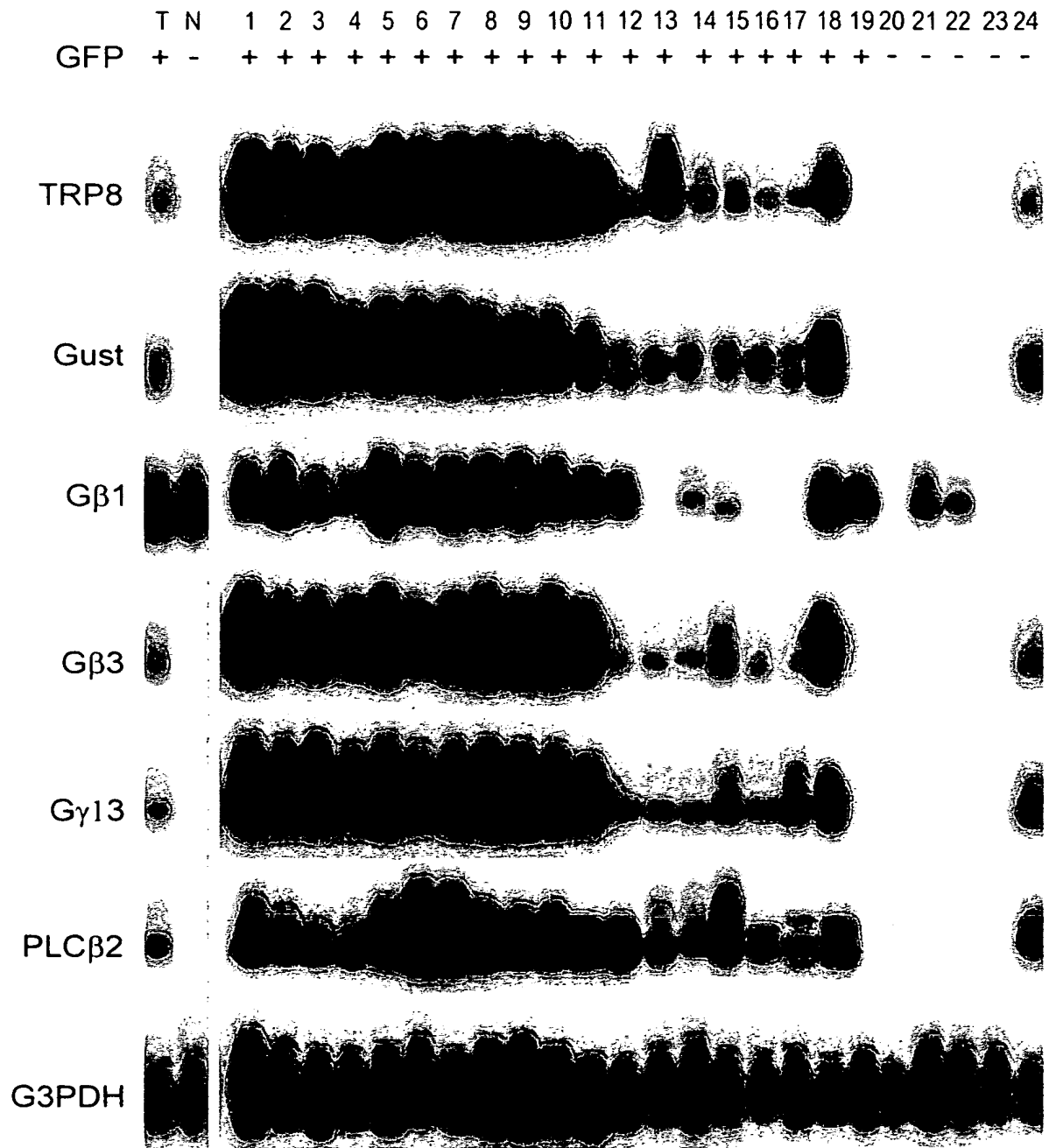


FIG.10

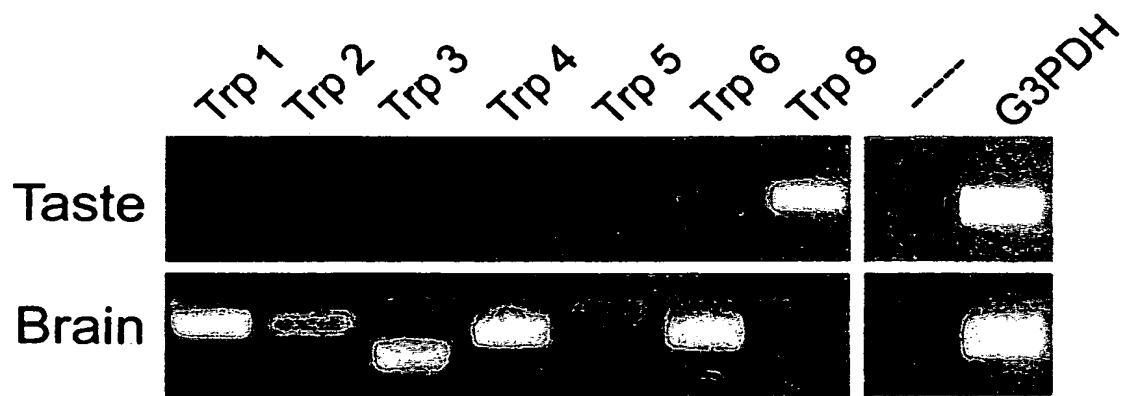


FIG. 11

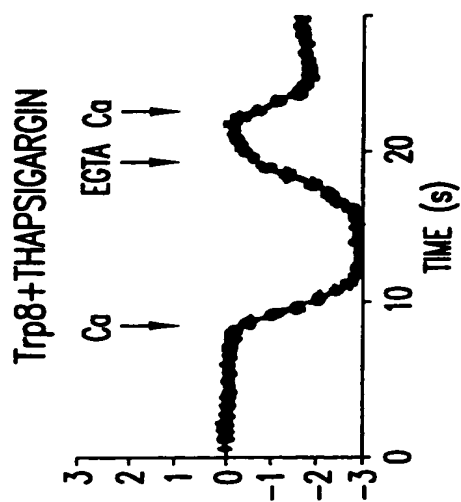


FIG. 12A

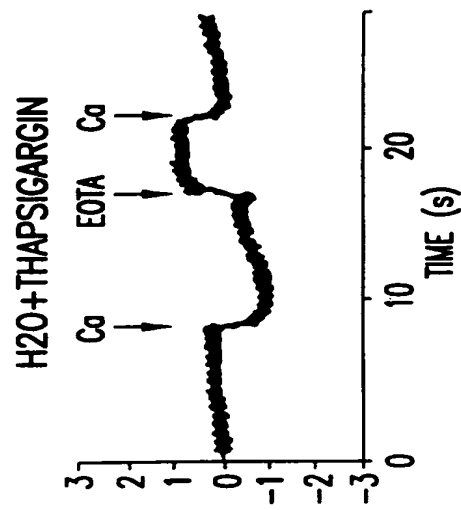


FIG. 12C

I-V RELATIONSHIP IN Trp8 INJECTED OOCYTES

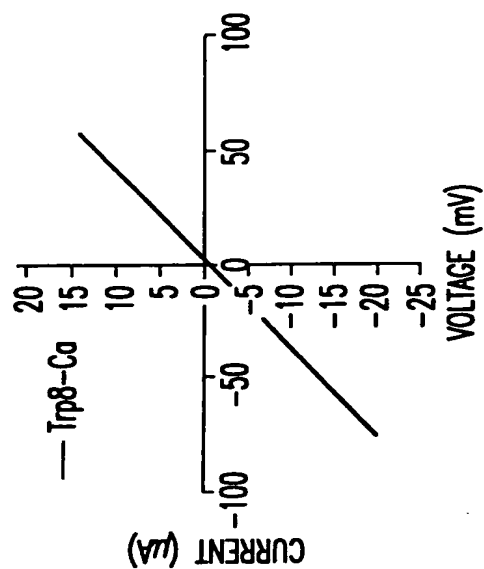


FIG. 12B

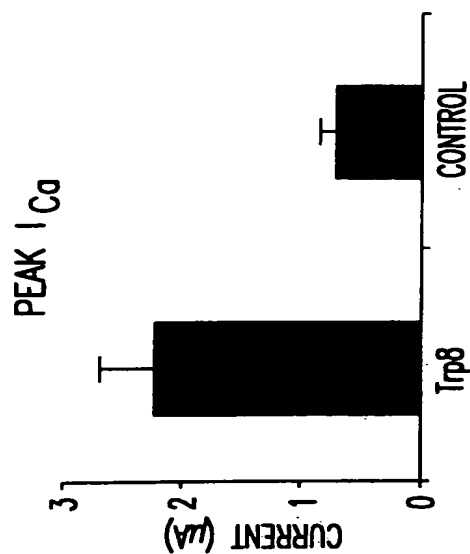


FIG. 12D

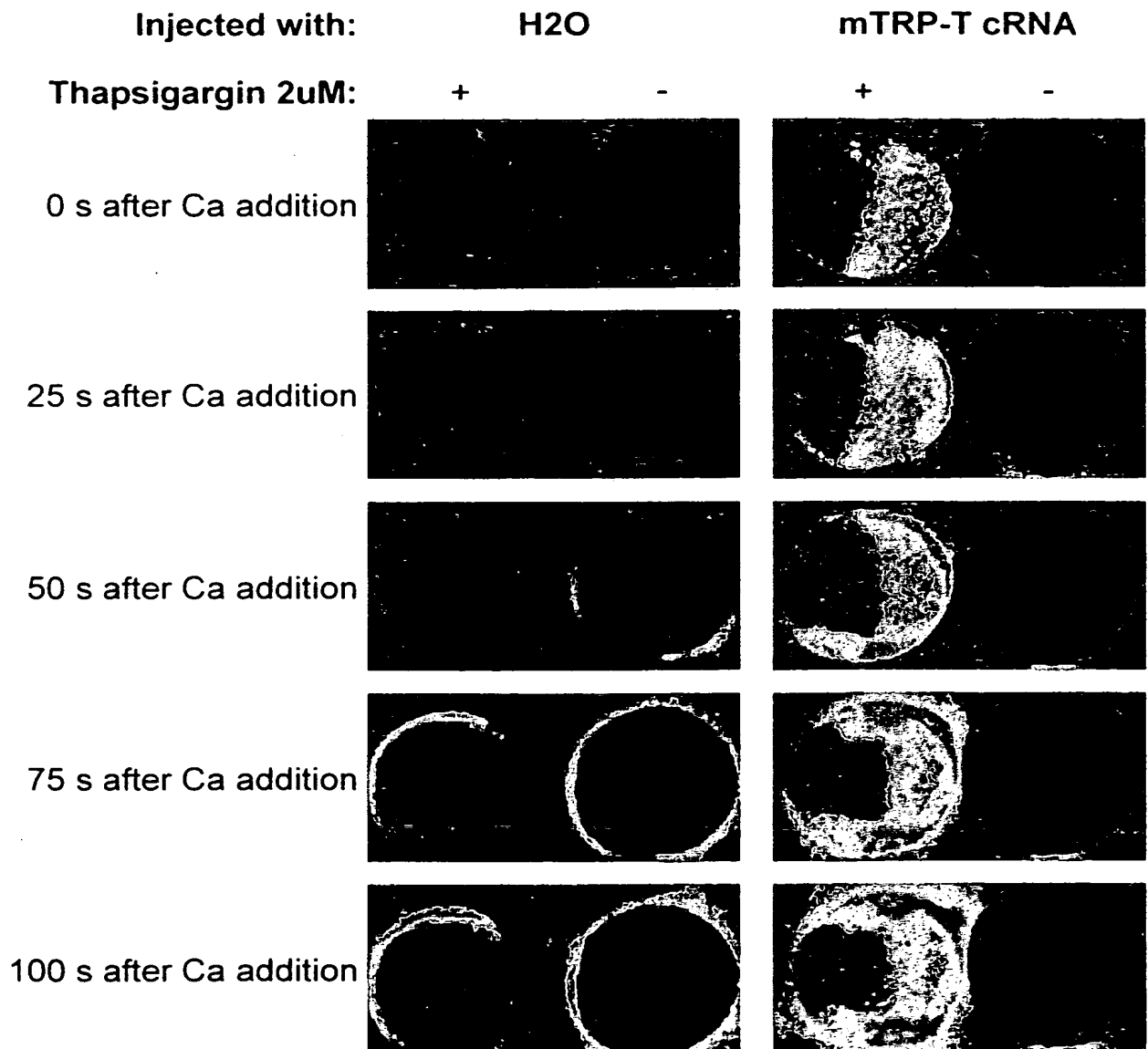


FIG.13

TRANSDUCTION OF TASTE STIMULI

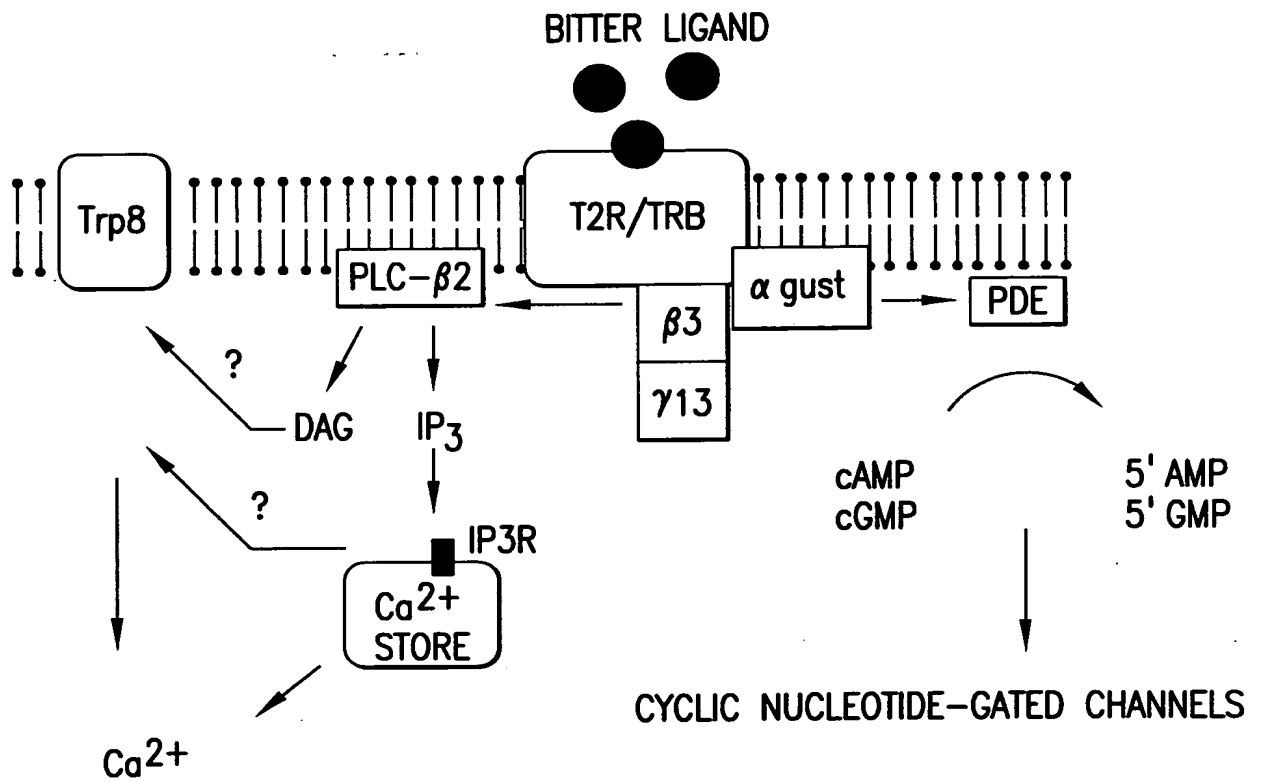


FIG. 14